

**Other sequence(s)
detected in
Swiss-Prot**

1.

Last update

November 1995 / Pattern and text revised.

References

[1]

Futai M., Noumi T., Maeda M.
Annu. Rev. Biochem. 58:111-136(1989).

[2]

Senior A.E.
Physiol. Rev. 68:177-231(1988).

[3]

Miki J., Maeda M., Mukohata Y., Futai M.
FEBS Lett. 232:221-226(1988).

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General information about the entry

Entry name	ATPG_ECOLI	
Primary accession number	P00837	
Secondary accession number	P00838	
Entered in Swiss-Prot in	Release 01, July 1986	
Sequence was last modified in	Release 01, July 1986	
Annotations were last modified in	Release 42, September 2003	
Name and origin of the protein		
Protein name	ATP synthase gamma chain	
Synonym	EC 3.6.3.14	
Gene name	ATPG or UNCG or PAPC or B3733 or C4659 or Z5231 or ECS4675 or SF3813	
From	Escherichia coli Escherichia coli O6 Escherichia coli O157:H7 Shigella flexneri	[TaxID: 562] [TaxID: 217992] [TaxID: 83334] [TaxID: 623]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	

References

[1]	SEQUENCE FROM NUCLEIC ACID. SPECIES =E.coli; MEDLINE=85121806; PubMed=6395859; [NCBI, ExPASy, EBI, Israel, Japan] <u>Walker J.E.</u> , <u>Gay N.J.</u> , <u>Saraste M.</u> , <u>Eberle A.N.</u> : "DNA sequence around the Escherichia coli unc operon. Completion of the sequence of a 17 kilobase segment containing <i>asnA</i> , <i>oriC</i> , <i>unc</i> , <i>glmS</i> and <i>phoS</i> ."; <i>Biochem. J.</i> 224:799-815(1984).
[2]	SEQUENCE FROM NUCLEIC ACID. SPECIES =E.coli; MEDLINE=82059507; PubMed=6272217; [NCBI, ExPASy, EBI, Israel,

Japan]

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"The atp operon: nucleotide sequence of the genes for the gamma, beta, and epsilon subunits of *Escherichia coli* ATP synthase.";

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[3] SEQUENCE FROM NUCLEIC ACID.

SPECIES=*E.coli*;

MEDLINE=82134798; **PubMed**=6277310; [NCBI, ExPASy, EBI, Israel, Japan]

Kanazawa H., Kayano T., Mabuchi K., Futai M.:

"Nucleotide sequence of the genes coding for alpha, beta and gamma subunits of the proton-translocating ATPase of *Escherichia coli*.";

Biochem. Biophys. Res. Commun. 103:604-612(1981).

[4] SEQUENCE FROM NUCLEIC ACID.

SPECIES=*E.coli*;

STRAIN=K12 / MG1655;

MEDLINE=93315143; **PubMed**=7686882; [NCBI, ExPASy, EBI, Israel, Japan]

Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.:

"DNA sequence and analysis of 136 kilobases of the *Escherichia coli* genome: organizational symmetry around the origin of replication.";

Genomics 16:551-561(1993).

[5] SEQUENCE FROM NUCLEIC ACID.

SPECIES=*E.coli*;

STRAIN=O6:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; **PubMed**=12471157; [NCBI, ExPASy, EBI, Israel, Japan]

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D.,

Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F.,

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"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic *Escherichia coli*.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

[6] SEQUENCE FROM NUCLEIC ACID.

SPECIES=E.coli;
STRAIN=O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; **PubMed**=11206551; [NCBI, ExPASy, EBI, Israel, Japan]

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
 "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7."; *Nature* 409:529-533(2001).

[7] **SEQUENCE FROM NUCLEIC ACID.**

SPECIES=E.coli;
STRAIN=O157:H7 / RIMD 0509952;
MEDLINE=21156231; **PubMed**=11258796; [NCBI, ExPASy, EBI, Israel, Japan]

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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[8] **SEQUENCE OF 261-287 FROM NUCLEIC ACID.**

SPECIES=E.coli;
MEDLINE=90202983; **PubMed**=2138624; [NCBI, ExPASy, EBI, Israel, Japan]

Iwamoto A., Miki J., Maeda M., Futai M.;

"H(+)-ATPase gamma subunit of *Escherichia coli*. Role of the conserved carboxyl-terminal region.";
J. Biol. Chem. 265:5043-5048(1990).

[9] **SEQUENCE FROM NUCLEIC ACID.**

SPECIES=S.flexneri;
STRAIN=301 / Serotype 2a;
MEDLINE=22272406; **PubMed**=12384590; [NCBI, ExPASy, EBI, Israel,

Japan]

Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J.,
Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue
Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He
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[10] X-RAY CRYSTALLOGRAPHY (4.4 ANGSTROMS).

SPECIES=*E.coli*;

MEDLINE=20040613; **PubMed**=10570135; [NCBI, ExPASy, EBI, Israel,
Japan]

Hausrath A.C., Grueber G., Matthews B.W., Capaldi R.A.:

"Structural features of the gamma subunit of the *Escherichia coli* F(1) ATPase revealed by a 4.4-A resolution map obtained by X-ray crystallography.";

Proc. Natl. Acad. Sci. U.S.A. 96:13697-13702(1999).

Comments

FUNCTION. PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CF(0) COMPLEX.

CATALYTIC ACTIVITY: ATP + H₂O + H⁺(In) = ADP + phosphate + H⁺(Out).

SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.

SIMILARITY: Belongs to the ATPase gamma chain family.

CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS AND VARIOUS OTHER ERRORS.

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Cross-references

EMBL	X01631; CAA25781.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
	J01594; AAA24736.1; ALT_FRAME. [EMBL / GenBank / DDBJ] [CodingSequence]
	V00267; CAA23526.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
	M25464; AAA83874.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
	V00312; CAA23597.1; ALT_FRAME. [EMBL / GenBank / DDBJ] [CodingSequence]
	L10328; AAA62085.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
	AE000450; AAC76756.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
	AE016769; AAN83091.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
	AE005605; AAG58936.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
	AP002566; BAB38098.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
PIR	M34095; AAA24742.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
	AE015388; AAN45253.1; -. [EMBL / GenBank / DDBJ] [CodingSequence]
	A01038; PWECG. C91213; C91213. D86059; D86059.
PDB	1D8S; 03-DEC-99. [ExPASy / RCSB]
	1FS0; 01-MAY-01. [ExPASy / RCSB]
	Detailed list of linked structures.

EcoGene	EG10104 ; atpG.
EcoCyc	EG10104 ; atpG.
CMR	P00837; B3733.
InterPro	IPR000131 ; ATPase_gamma. Graphical view of domain structure .
Pfam	PF00231 ; ATP-synt; 1.
PRINTS	PR00126 ; ATPASEGAMMA.
TIGRFAMs	TIGR01146 ; ATPsyn_F1gamma; 1.
PROSITE	PS00153 ; ATPASE_GAMMA; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P00837.
ProtoNet	P00837.
ProtoMap	P00837.
PRESAGE	P00837.
DIP	P00837.
ModBase	P00837.
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Keywords

[ATP synthesis](#); [CF\(1\)](#); [Hydrogen ion transport](#); [Hydrolase](#); [3D-structure](#); [Complete proteome](#).

Features

None

Sequence information

Length: 287	Molecular weight:	CRC64: 2417A4B8FBDB8EF8 [This is a checksum on the sequence]
AA	31577 Da	

10	20	30	40	50	60	
MAGAKEIRSK	IASVQNTQKI	TKAMEMVAAS	KMRKSQDRMA	ASRPYAETMR	KVIGHLAHGN	
70	80	90	100	110	120	
LEYKHPYLED	RDVKRKGVLV	VSTDRLGLCGG	LNINLFKKLL	AEMKTWTDKG	VQCDLAMIGS	
130	140	150	160	170	180	
KGVSFFNSVG	GNVVAQVTGM	GDNPSLSELI	GPVKVMLQAY	DEGRLLDKLYI	VSNKFINTMS	
190	200	210	220	230	240	
QVPTISQLLP	LPASDDDDLK	HKSWDYLYEP	DPKALLDTLL	RRYVESQVYQ	GVVENLASEQ	
250	260	270	280			
AARMVAMKAA	TDNGGSLIKE	LQLVYNKARQ	ASITQELTEI	VSGAAAV		

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[PeptideMass](#), [PeptideCutter](#),
[Dotlet](#) (Java)



[ScanProsite](#),
[MotifScan](#)



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NCBI BLAST program reference [PMID:9254694] :

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query length: 289 AA
 Date run: 2003-06-11 14:57:44 UTC+0100 on sib-blast.unil.ch
 Program: NCBI BLASTP 2.2.5 [Nov-16-2002]
 Database: XXtremblnew; XXtrembl; XXswissprot
 1,135,895 sequences; 361,048,751 total letters
 Swiss-Prot Release 41.11 of 06-Jun-2003
 TrEMBL Release 23.15 of 06-Jun-2003
 TrEMBL_new of 06-Jun-2003

Taxonomic view	NiceBlast view	Printable view
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List of potentially matching sequences

Send selected sequences to	Clustal W (multiple alignment)	▼	Submit Query
<input type="button" value="Select up to..."/>			

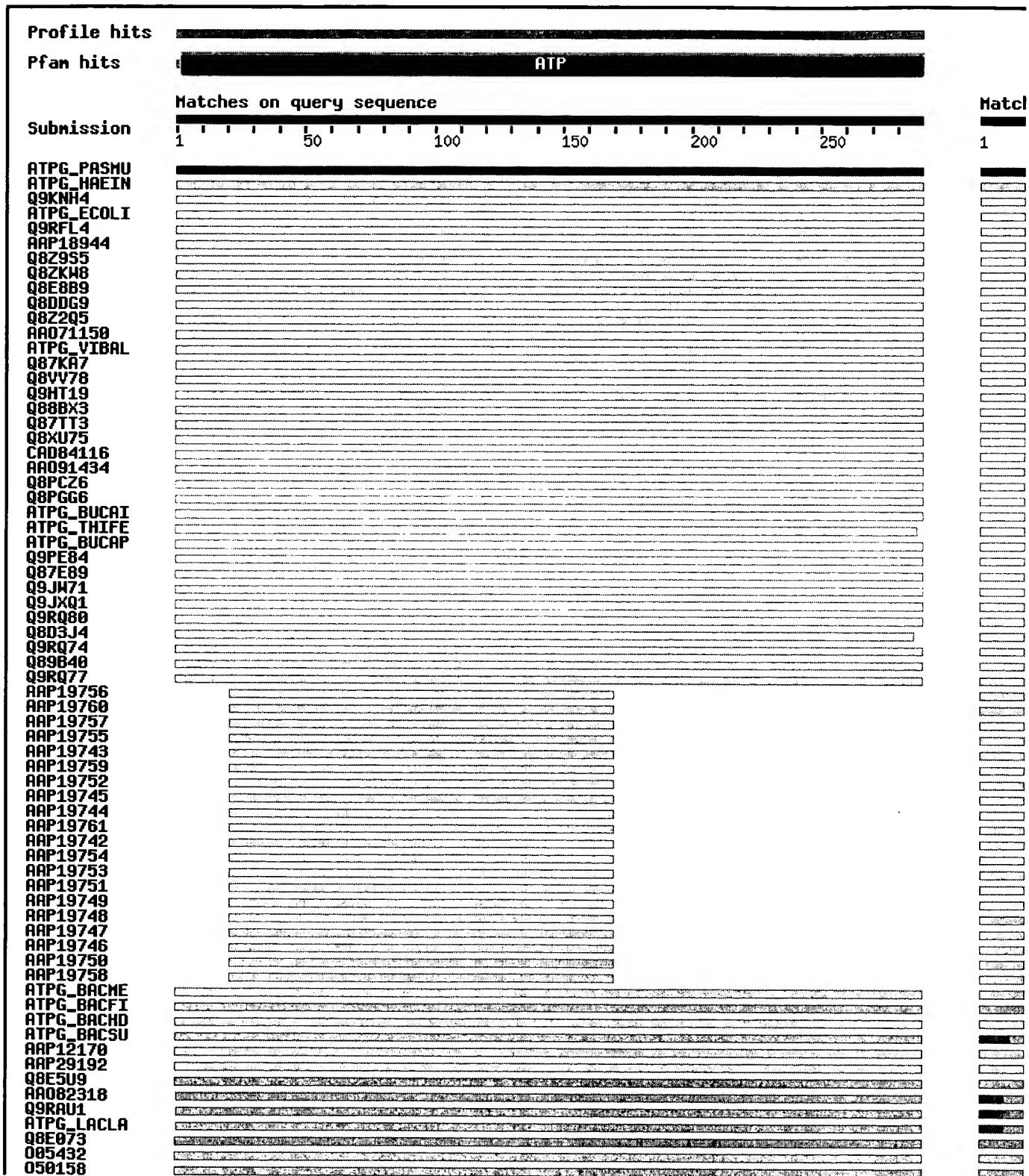
Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp Q9L6B6	ATPG_PASMU ATP synthase gamma chain (EC 3.6.3.14) [ATP...]	555	e-157
<input type="checkbox"/>	sp P43716	ATPG_HAEIN ATP synthase gamma chain (EC 3.6.3.14) [ATP...]	456	e-127
<input type="checkbox"/>	tr Q9KNH4	ATP synthase F1, gamma subunit [VC2765] [Vibrio cholerae]	388	e-107
<input type="checkbox"/>	sp P00837	ATPG_ECOLI ATP synthase gamma chain (EC 3.6.3.14) [ATP...]	385	e-106
<input type="checkbox"/>	tr Q9RFL4	ATP synthase subunit gamma [ATPG] [Salmonella typhimur...]	385	e-106
<input type="checkbox"/>	tn AAP18944	Membrane-bound ATP synthase, F1 sector, gamma-subuni...	385	e-106
<input type="checkbox"/>	tr Q8Z9S5	ATP synthase gamma subunit protein (EC 3.6.1.34) (Memb...)	384	e-106
<input type="checkbox"/>	tr Q8ZKW8	Membrane-bound ATP synthase, F1 sector, gamma-subunit ...	384	e-106

<input type="checkbox"/>	tr Q8E8B9	ATP synthase F1, gamma subunit [ATPG] [Shewanella onei...]	<u>382</u>	e-105
<input type="checkbox"/>	tr Q8DDG9	ATP synthase F1, gamma subunit [VV11020] [Vibrio vulni...]	<u>381</u>	e-105
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<input type="checkbox"/>	tn AAO71150	ATP synthase gamma subunit [atpG] [Salmonella typhi]	<u>380</u>	e-104
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<input type="checkbox"/>	tr Q87KA7	ATP synthase F1, gamma subunit [VP3070] [Vibrio paraha...]	<u>377</u>	e-104
<input type="checkbox"/>	tr Q8VV78	F0F1-ATPase subunit gamma [ATPG] [Colwellia maris (Vib...]	<u>362</u>	3e-99
<input type="checkbox"/>	tr Q9HT19	ATP synthase gamma chain [ATPG] [Pseudomonas aeruginosa]	<u>360</u>	1e-98
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<input type="checkbox"/>	tr Q87TT3	ATP synthase F1, gamma subunit [ATPG] [Pseudomonas syr...]	<u>344</u>	6e-94
<input type="checkbox"/>	tr Q8XU75	Probable ATP synthase gamma chain protein (EC 3.6.1.34...)	<u>344</u>	6e-94
<input type="checkbox"/>	tn CAD84116	ATP synthase gamma subunit (EC 3.6.3.14) [atpG] [Nit...]	<u>343</u>	1e-93
<input type="checkbox"/>	tn AAO91434	ATP synthase, F1 gamma subunit [atpG] [Coxiella burn...]	<u>328</u>	5e-89
<input type="checkbox"/>	tr Q8PCZ6	ATP synthase gamma chain [ATPG] [Xanthomonas campestris...]	<u>325</u>	4e-88
<input type="checkbox"/>	tr Q8PGG6	ATP synthase gamma chain [ATPG] [Xanthomonas axonopodi...]	<u>322</u>	3e-87
<input type="checkbox"/>	sp P57123	ATPG_BUCAI ATP synthase gamma chain (EC 3.6.3.14) [ATP...]	<u>315</u>	5e-85
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<input type="checkbox"/>	sp O51873	ATPG_BUCAP ATP synthase gamma chain (EC 3.6.3.14) [ATP...]	<u>308</u>	5e-83
<input type="checkbox"/>	tr Q9PE84	ATP synthase, gamma chain [XF1144] [Xylella fastidiosa]	<u>307</u>	9e-83
<input type="checkbox"/>	tr Q87E89	ATP synthase gamma chain [ATPG] [Xylella fastidiosa (s...]	<u>306</u>	2e-82
<input type="checkbox"/>	tr Q9JW71	ATP synthase gamma chain (EC 3.6.1.34) [ATPG] [Neisser...]	<u>293</u>	1e-78
<input type="checkbox"/>	tr Q9JXQ1	ATP synthase F1, gamma subunit [NMB1935] [Neisseria me...]	<u>293</u>	2e-78
<input type="checkbox"/>	tr Q9RQ80	Gamma subunit of membrane-bound ATP synthase [ATPG] [B...]	<u>291</u>	6e-78
<input type="checkbox"/>	tr Q8D3J4	AtpG protein [ATPG] [Wigglesworthia brevipalpis]	<u>270</u>	2e-71
<input type="checkbox"/>	tr Q9RQ74	Gamma subunit of membrane-bound ATP synthase [ATPG] [B...]	<u>266</u>	2e-70
<input type="checkbox"/>	tr Q89B40	ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Buchner...]	<u>261</u>	9e-69
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<input type="checkbox"/>	tn AAP19757	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...]	<u>228</u>	9e-59
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<input type="checkbox"/>	tn AAP19743	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...]	<u>228</u>	9e-59
<input type="checkbox"/>	tn AAP19759	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...]	<u>227</u>	1e-58
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<input type="checkbox"/>	tn AAP19754	ATP synthase F1 epsilon subunit (Fragment) [atpG] [H...]	<u>226</u>	2e-58
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<input type="checkbox"/>	<u>sp P22482</u>	ATPG_BACFI ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>209</u>	4e-53
<input type="checkbox"/>	<u>sp Q9K6H4</u>	ATPG_BACHD ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>208</u>	5e-53
<input type="checkbox"/>	<u>sp P37810</u>	ATPG_BACSU ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>207</u>	9e-53
<input type="checkbox"/>	<u>tn AAP12170</u>	ATP synthase gamma chain (EC 3.6.3.14) [BC5307]	[Bac...]	<u>207</u>	2e-52
<input type="checkbox"/>	<u>tn AAP29192</u>	ATP synthase F1, gamma subunit [atpG]	[Bacillus anth...]	<u>207</u>	2e-52
<input type="checkbox"/>	<u>tr Q8E5U9</u>	H+-transporting ATP synthase gamma chain [ATPG]	[Strep...]	<u>205</u>	6e-52
<input type="checkbox"/>	<u>tn AAO82318</u>	ATP synthase F1, gamma subunit [atpG]	[Enterococcus ...]	<u>205</u>	6e-52
<input type="checkbox"/>	<u>tr Q9RAU1</u>	H+-ATPase cytoplasmic F1-part gamma-subunit (H+-ATPase...)		<u>204</u>	1e-51
<input type="checkbox"/>	<u>sp Q9CER9</u>	ATPG_LACLA ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>204</u>	1e-51
<input type="checkbox"/>	<u>tr Q8E073</u>	ATP synthase F1, gamma subunit [ATPG]	[Streptococcus a...]	<u>202</u>	3e-51
<input type="checkbox"/>	<u>tr O05432</u>	ATP synthase subunit gamma [ATPG]	[Moorella thermoacet...]	<u>201</u>	7e-51
<input type="checkbox"/>	<u>tr O50158</u>	Proton-translocating ATPase, gamma subunit [ATPG]	[Str...]	<u>201</u>	1e-50
<input type="checkbox"/>	<u>tr Q8EM82</u>	H(+) -transporting ATP synthase gamma chain (EC 3.6.1.3...)		<u>197</u>	9e-50
<input type="checkbox"/>	<u>tr Q9A0I8</u>	Putative proton-translocating ATPase, gamma subunit (E...)		<u>197</u>	9e-50
<input type="checkbox"/>	<u>sp P09222</u>	ATPG_BACP3 ATP synthase gamma chain precursor (EC 3.6....)		<u>196</u>	2e-49
<input type="checkbox"/>	<u>tr Q8K827</u>	Putative proton-translocating ATPase gamma subunit [SP...]		<u>196</u>	2e-49
<input type="checkbox"/>	<u>tr Q97PT5</u>	ATP synthase F1, gamma subunit (Proton-translocating A...)		<u>196</u>	3e-49
<input type="checkbox"/>	<u>tr Q52412</u>	TF1-gamma subunit [thermophilic bacterium PS3]		<u>196</u>	4e-49
<input type="checkbox"/>	<u>tr Q8RKV3</u>	H+-ATPase cytoplasmic F1-part gamma-subunit [ATPG]	[St...]	<u>194</u>	1e-48
<input type="checkbox"/>	<u>sp P12408</u>	ATPG_ANASP ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>193</u>	2e-48
<input type="checkbox"/>	<u>tr Q8CNJ6</u>	ATP synthase gamma chain [SE1701] [Staphylococcus epid...]		<u>193</u>	2e-48
<input type="checkbox"/>	<u>tr Q927W3</u>	AtpG protein [ATPG] [Listeria monocytogenes, Listeria ...]		<u>193</u>	2e-48
<input type="checkbox"/>	<u>sp P17253</u>	ATPG_SYNY3 ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>192</u>	4e-48
<input type="checkbox"/>	<u>tr Q99SF4</u>	ATP synthase gamma chain [ATPG]	[Staphylococcus aureus...]	<u>192</u>	4e-48
<input type="checkbox"/>	<u>sp P08450</u>	ATPG_SYNP6 ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>191</u>	1e-47
<input type="checkbox"/>	<u>tn AAO43198</u>	Chloroplast ATPase gamma subunit precursor [AtpC]	[P...]	<u>190</u>	2e-47
<input type="checkbox"/>	<u>sp P43452</u>	ATPG_ENTHR ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>190</u>	2e-47
<input type="checkbox"/>	<u>sp P41010</u>	ATPG_BACCA ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>190</u>	2e-47
<input type="checkbox"/>	<u>sp P29710</u>	ATPG_PROMO ATP synthase gamma chain, sodium ion specif...		<u>189</u>	3e-47
<input type="checkbox"/>	<u>tr Q8KAW9</u>	ATP synthase F1, gamma subunit [ATPG]	[Chlorobium tepi...]	<u>189</u>	3e-47
<input type="checkbox"/>	<u>tr Q8DLU1</u>	H+-transporting ATP synthase gamma chain [ATPC]	[Synec...]	<u>188</u>	6e-47
<input type="checkbox"/>	<u>sp Q05384</u>	ATPG_SYNP1 ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>188</u>	8e-47
<input type="checkbox"/>	<u>sp P42007</u>	ATPG_BACST ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>188</u>	8e-47
<input type="checkbox"/>	<u>sp Q06908</u>	ATPG_ODOSI ATP synthase gamma chain, chloroplast precu...		<u>187</u>	1e-46
<input type="checkbox"/>	<u>tr Q9ZJ02</u>	Proton-translocating ATPase gamma subunit [Streptococc...]		<u>187</u>	2e-46
<input type="checkbox"/>	<u>sp P95788</u>	ATPG_STRMU ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>186</u>	2e-46
<input type="checkbox"/>	<u>tr Q8KRU9</u>	Subunit gamma [ATPG]	[Ilyobacter tartaricus]	<u>184</u>	8e-46
<input type="checkbox"/>	<u>tr Q8RGE1</u>	ATP synthase gamma chain, sodium ion specific (EC 3.6....)		<u>184</u>	1e-45
<input type="checkbox"/>	<u>sp Q41075</u>	ATPG_PHATR ATP synthase gamma chain, chloroplast precu...		<u>183</u>	2e-45
<input type="checkbox"/>	<u>sp Q10597</u>	ATPG_MYCTU ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>182</u>	4e-45
<input type="checkbox"/>	<u>sp P56082</u>	ATPG_HELPY ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>181</u>	7e-45
<input type="checkbox"/>	<u>sp Q9ZK80</u>	ATPG_HELPJ ATP synthase gamma chain (EC 3.6.3.14)	[ATP...]	<u>179</u>	3e-44
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<input type="checkbox"/>	<u>tr Q8A9U6</u>	ATP synthase gamma chain [BT0719]	[Bacteroides thetaio...]	<u>178</u>	6e-44

Graphical overview of the alignments

[Click here](#)to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMsnew(use ScanProsite for more details about PROSITE matches)

PCL XL error

Subsystem: KERNEL
Error: IllegalOperatorSequence
Operator: SetClipToPage
Position: 9096

IPB000131: ATPase_gamma

ATP synthase gamma subunit

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- [Block number IPB000131C](#)
- [Block number IPB000131D](#)
- [Block number IPB000131E](#)
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Block IPB000131A

ID	ATPase_gamma; BLOCK				
AC	IPB000131A; distance from previous block=(0, 62)				
DE	ATP synthase gamma subunit				
BL	ITM; width=32; seqs=82; 99.5%=1504; strength=1376				
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ATPG PROMO P29710	(3) GKEIKSRISSVQSTRQITKAMEIVSSTKFKKF	22			
ATPG RHORU P07227	(4) LKDLRSLRTSVKSTQKITSAMKVAASRLRRA	10			
ATPG RICPR O50289	(4) LKQLRTRIKSVKSTQKITKAMQLVSASKMTKI	12			
ATPG ANASP P12408	(4) LKSIRDRIQSVKNTKKITEAMRLVAAARVRA	14			
ATPG RHOBL P05436	(4) LKDLKNRIGSVKNTRKITKAMQMVAAKLRRRA	8			
ATPG RHOCA P72246	(4) LKDLKNRIVSVKNTRKITKAMQMVAANIRRA	15			
ATPG SPIPL P50006	(3) LKAIRDRIQSVKNTKKITEAMRLVASA KVRA	10			
ATPG SYNP1 Q05384	(4) LKAIRDRIKTIKDTRKITEAMRLVAAAKVRA	17			
ATPG SYNP6 P08450	(4) LKAIRDRIKSVRNTRKITEAMRLVAAAKVRA	13			
ATPG SYNY3 P17253	(4) LKAIRDRIQSVKNTKKITEAMRLVAAAKVRA	9			
ATP1 ARATH Q01908	(53) LRELDRRIDSVKNTQKITEAMKLVAAAKVRA	8			
ATP2 ARATH Q01909	(63) IRELRERIDSVKNTQKITEAMRLVAAARVRA	12			
ATPG CHLRE P12113	(37) LKEVRDRIASVKNTQKITDAMKLVAAAKVRA	12			
ATPG ODOSI Q06908	(59) ANAIRDRITSVKNTKKITMAMKLVAAAKVRA	11			
ATPG PEA P28552	(54) LKDLKNRIDSVKNTQKITEAMKLVAAAKVRA	8			
ATPG PHATR Q41075	(58) ANAIRDRITSVKNTRKITMAMKLVRAAPKVR	43			
ATPG SPIOL P05435	(44) LRELDRDRIGSVKNTQKITEAMKLVAAAKVRA	8			
ATPG TOBAC P29790	(57) LRDLRDRIESVKNTQKITEAMKLVAAAKVRA	8			
ATPG BACCA P41010	(7) LRDIKTRINATKKTSQITKAMEMVSTS KLNRA	10			
ATPG BACFI P22482	(4) LRDIQGRITSTKKTKQITKAMQMVSAAKLNRA	12			
ATPG BACP3 P09222	(7) LRDIKTRINATKKTSQITKAMEMVLTS KLNRA	15			
ATPG BUCAI P57123	(4) TKEIKKNKIVSVTNTKKITKAMEMVAVSKMRKT	12			
ATPG BUCAP O51873	(4) KKEIKDQIISVTNTKKITKAMEMVAVSKMRKT	17			
ATPG ECOLI P00837	(4) AKEIRSKIASVQNTQKITKAMEMVAASKMRKS	8			
ATPG THIFE P41169	(4) AKEIRGQIKSVKNTRKITRAMEMVAASKMRRA	12			
ATPG VIBAL P12990	(4) AKEIRNKIGSVKSTQKITKAMEMVAASKMRSS	8			
ATPG MYCGE P47640	(4) IQEIKRMMNTVKSTIKITNAMKMSRAKFIKF	26			
ATPG MYCPN Q50330	(4) IQEIKRKMTTVQSTIKITNAMKMSRAKFVRF	22			
ATP3 ARATH Q96250	(45) TQVVRNRMKSVKNIQKITKAMKVAASKLRAV	24			
ATP3 IPOBA P26360	(48) TQVVRNRMKSVKNIQKITKAMKVAASKLRAI	20			
ATPG BOVIN P05631	(28) LKDITRRLKSIKNIQKITKSMKVAAKYARA	13			
ATPG HUMAN P36542	(28) LKDITRRLKSIKNIQKITKSMKVAAKYARA	13			
ATPG RAT P35435	(3) LKDITRRLKSIKNIQKITKSMKVAAKYARA	13			

ATPG KLULA	P49377	(20)	LREIETRLSIKNIKIEKITKTMKIVASTRLSKA	24
ATPG YEAST	P38077	(36)	LKEVEMRLSIKNIKIEKITKTMKIVASTRLSKA	28
ATPG ACEWO	P50005	(4)	VQDIKPRIKSVNSTMQITHAMELVASAKLRKS	21
ATPG BACME	P20602	(4)	LRDIQTRITSTKKTQITKAMEMVSAAKLNRA	11
ATPG BACST	P42007	(7)	LRDIKTRINATKKTQITKAMEMVSTSKLNRA	10
ATPG BACSU	P37810	(7)	LRDIKSITSTKKTQITKAMQMVSAAKLNRA	9
ATPG ENTHR	P43452	(5)	LNEIKTRIASTKKTQITRAMQVSASKLTKS	11
ATPG HAEIN	P43716	(4)	AKEIKTKIASVQSTQKITKAMEMVATSKMRKT	8
ATPG HELPY	P56082	(4)	LRDIRKKIGSVKNTQKITHAMKLVSTSKLRKA	10
ATPG HELPJ	Q9ZK80	(4)	LRDIRKKIGSVKNTQKITHAMKLVSTSKLRKA	14
ATPG MYCLE	P45824	(5)	LRELGRGRISVGSIKITKAQELIATSRIARA	18
ATPG MYCTU	Q10597	(5)	LRELGRGRISAGSIKKITKAQELIATSRIARA	27
ATPG PASMU	Q9L6B6	(4)	AKEIRTKIASVNSTQKITKAMEMVAASKMRKT	8
ATPG STRLI	P50007	(4)	LRVYKRRIRSVTATKKITKAMEMIAASRVVKA	17
ATPG STRMU	P95788	(5)	LSEIKVIRTSTQKTGKITSAMKMSSAKLVKS	20
ATPG DROME	Q01666	(29)	LKMISIRLKSVKNIQKITQSMKMVSAAKYARA	32
O74754		(34)	LKEIEQRLSIKNIKIEKITKTIKTVQATKLTRA	38
Q9NE84		(5)	LRLYKEKLEGYNRFYSIVKTIKAMVMTMAKFRQA	100
O21267		(4)	TKDFKNRIKSITSIRKITKAMKVAASKLRQA	20
Q9G8R3		(4)	PKKLLQLKSYERFKLLTKAIQMVALSQLSGL	93
O50141		(4)	MKDVKRRIKSVESTMQITKAMQLVASSKMRKA	14
O50158		(5)	LSEIKGKIIISTQKTSHITGAMQMVSAAKLTKS	20
O67829		(6)	PRDIKRKIQGIKNTKRITNAMKVVSAAKLRKA	27
O05432		(4)	MRDLKRRIRSVQSTQKITRAMKVAASKLRKA	13
Q52412		(3)	LRDIKTRINATKKTQITKAMEMVLTSLNRA	15
Q9ZJ02		(5)	LNDIKNKIASTKNTQITNAMQMVSAAKLGKS	15
Q9Z688		(6)	LIIIKRRIKSITNTKKITNAMGLIATSNLRKS	35
Q9X1U6		(1)	MLQIKRKINATQSLMKITRAMEMVARAKVRKI	33
Q9RQ80		(4)	IKEIKTQITSVVNTKKITKAMEMVAISKMRKT	18
Q9RQ77		(4)	KKEIKNKNINCISNTKKITKAMEMVSIAKMKKS	22
Q9RQ74		(4)	IKEVRNKKCITNTQKITKAMEMVSISKMKA	17
Q9RGY2		(5)	LLELKRKIASVKQTGKITEAMRMSASKLNQT	22
Q9RFL4		(4)	AKEIRSKIASVQNTQKITKAMEMVAASKMRKS	8
Q9RAU1		(5)	LNEIKTKIASTKKTQITGAMQMVSAAKLQKA	13
Q9PR14		(3)	LDAMKRKINSVQTTAKITNAMKLVATAKLKRQ	38
Q9PJ20		(4)	LKEIKRKISVHNTQKTTNAMKLVSTAKLKKA	25
Q9PE84		(4)	GREIKSKIKSVQNTRKVTRALEMVSASKIRKA	34
Q9KNH4		(4)	AKEIRTKIGSVKSTQKITKAMEMVAASKMRRS	8
Q9K6H4		(4)	LRDIQRIINSTKKTQITKAMEMVSAAKLNRS	10
Q9K4D4		(5)	LRVYKRRIRSVTATKKITKAMEMIAASRVVKA	17
Q9JXQ1		(4)	GKEILTKIRSVQNTQKITKAMQMVSSTSKMRKT	12
Q9JW71		(4)	GKEILTKIRSVQNTQKITKAMQMVSSTSKMRKT	12
Q9HT19		(4)	AKEIRSKIASIKSTQKITNAMEKVAVSKMRKA	18
Q9FDR6		(4)	IRELDRDRIRSVNSTKKITKAQELIATSRTKA	16
Q9FAA4		(4)	IRELDRDRIRSVNSTKKITKAQELIATSRTKA	16
Q9CER9		(5)	LNEIKTKIASTKKTQITGAMQMVSAAKLQKA	13
Q9ERA8		(28)	LKDITRRLKSIKNIQKITKSMKMVAASKYARA	13
Q9D9D7		(28)	LKDITRRLKSIKNIQKITKSMKMVAASKYARA	13

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Block IPB000131B

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DE	ATP synthase gamma subunit
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ATPG BACFI	P22482 (73) VKKTGYIVVTSDKGLLAGGYNSSLIR 9
ATPG MYCGA	P33257 (74) STKRLWIVINTQLGLCGSYNTNVGK 49

<u>ATPG PROMO</u>	<u>P29710</u>	(73)	VKRIGIIVMTSDRGLCGGFNSSTLK	12
<u>ATPG RHOBL</u>	<u>P05436</u>	(74)	DQIHLVVMTSERGLCGGFNSTIVR	23
<u>ATPG RHOMA</u>	<u>P72246</u>	(76)	DKVHLLVIMTGERGLCGGFNANIAK	20
<u>ATPG RHORU</u>	<u>P07227</u>	(76)	DNVHLIVALTANRGLCGGFNGSIIR	24
<u>ATPG RICPR</u>	<u>O50289</u>	(77)	SKINLLIVMTSERGLCGMFNYSIIK	32
<u>ATPG SPIPL</u>	<u>P50006</u>	(74)	VKKVGLVVLAGNRGLCGAYNSNIK	19
<u>ATPG THIFE</u>	<u>P41169</u>	(73)	VKKAGFLVVTTDRGLCGGLNVNVLR	12
<u>ATPG ANASP</u>	<u>P12408</u>	(75)	VKSVGLLVISGDRGLCGGYNTNVIR	11
<u>ATPG SYNP1</u>	<u>Q05384</u>	(75)	VKTVALLVVTGDRGLCGGYNTNVIR	11
<u>ATPG SYNP6</u>	<u>P08450</u>	(75)	VKTVALLVVS GDRGLCGGYNSNVIR	11
<u>ATPG SYNY3</u>	<u>P17253</u>	(75)	PKAVALLVVTGDRGLCGGYNVNAIK	26
<u>ATPG BACCA</u>	<u>P41010</u>	(73)	VKKTGYLVITSDRGLAGAYNSNVVR	9
<u>ATPG BACP3</u>	<u>P09222</u>	(74)	VKKTGYLVITSDRGLAGAYNSNVLR	9
<u>ATPG BUCAI</u>	<u>P57123</u>	(73)	TNRIGMIIISTDRGLCGGLNTNLFK	16
<u>ATPG BUCAP</u>	<u>O51873</u>	(73)	DKRIGIIIVSTD RGLCGSLNTNLFK	12
<u>ATPG ECOLI</u>	<u>P00837</u>	(73)	VKRVGYLVVSTD RGLCGGLNINLFK	10
<u>ATPG VIBAL</u>	<u>P12990</u>	(73)	AKRVGYIIIVSTD RGLCGGLNINVFK	11
<u>ATPG MYCGE</u>	<u>P47640</u>	(69)	NQKTLWIMMSSSLGLCGQHNSNMNK	39
<u>ATPG MYCPN</u>	<u>Q50330</u>	(69)	NPKTLWVMMSSSLGLCGQHNTNMNK	39
<u>ATP1 ARATH</u>	<u>Q01908</u>	(124)	VKKVALVVVTGDRGLCGGFNNFIK	11
<u>ATP2 ARATH</u>	<u>Q01909</u>	(134)	VKRVALVVVTGDKGLCGGFNNAVTK	18
<u>ATPG CHLRE</u>	<u>P12113</u>	(108)	VKSVLLVVLTGDRGLCGGYNNFIK	14
<u>ATPG PEA</u>	<u>P28552</u>	(125)	VKKVALVVCTGDRGLCGGFNNAILK	17
<u>ATPG SPIOL</u>	<u>P05435</u>	(115)	VKKVALMVVTGDRGLCGGFNNMLK	30
<u>ATPG TOBAC</u>	<u>P29790</u>	(128)	VKKVALVVVTGDRGLCGGFNNYLIK	15
<u>ATPG ODOSSI</u>	<u>Q06908</u>	(130)	VSKVTLVVITGDRGLCGGYNSFMK	17
<u>ATPG PHATR</u>	<u>Q41075</u>	(130)	VKKVTLVITGDRGLCGGYNSFMK	15
<u>ATP3 ARATH</u>	<u>Q96250</u>	(102)	VKKSVVVTLSSDKGLCGGINSTVVK	20
<u>ATP3 IPOBA</u>	<u>P26360</u>	(105)	VKKNVIITIISSDKGLCGGINSTSVK	21
<u>ATPG BOVIN</u>	<u>P05631</u>	(88)	KKKHLLIIGVSSDRGLCGAIHSSVAK	14
<u>ATPG HUMAN</u>	<u>P36542</u>	(88)	KKKHLLIIGVSSDRGLCGAIHSSI AK	14
<u>ATPG RAT</u>	<u>P35435</u>	(63)	KKKHLLIIGVSSDRGLCGAIHSSVAK	14
<u>ATPG KLULA</u>	<u>P49377</u>	(81)	EKKDLIIIAITS DKGLCGSIHSQ LAK	20
<u>ATPG YEAST</u>	<u>P38077</u>	(102)	APKELIVAITSDKGLCGSIHSQ LAK	25
<u>ATPG ACEWO</u>	<u>P50005</u>	(73)	VKKTAYIIITGDKGLAGGYNVNVAK	11
<u>ATPG BACME</u>	<u>P20602</u>	(73)	VKKTGYIVITSDRGLAGAYNSNILR	9
<u>ATPG BACST</u>	<u>P42007</u>	(73)	VKKTGYLVITSDRGLAGAYNSNV R	9
<u>ATPG BACSU</u>	<u>P37810</u>	(76)	VKKTAYLVITSDRGLAGAFNSSVLR	9
<u>ATPG ENTHR</u>	<u>P43452</u>	(85)	VKKTGYIVITADGLVGGYNSSILK	22
<u>ATPG HAEIN</u>	<u>P43716</u>	(73)	VKKIGILVISTDRGMCGGLNVNLFK	15
<u>ATPG HELPY</u>	<u>P56082</u>	(81)	IKKVDIIFITADKGLCGGFNTNTIK	16
<u>ATPG HELPJ</u>	<u>Q9ZK80</u>	(81)	IKKVDIIFITADKGLCGGFNTNTIK	16
<u>ATPG MYCLE</u>	<u>P45824</u>	(74)	PKRAGVLVVSSDRGLCGAYNANVFR	11
<u>ATPG MYCTU</u>	<u>Q10597</u>	(74)	PKRAGVLVVSSDRGLCGAYNANIFR	11
<u>ATPG PASMU</u>	<u>Q9L6B6</u>	(73)	VKKVGMIVVSTD RGLCGGLNVNLFK	12
<u>ATPG STRLI</u>	<u>P50007</u>	(71)	PSRAAVLLLTS DRGLAGAFNSNSIK	17
<u>ATPG STRMU</u>	<u>P95788</u>	(76)	IKKTAYIVITS DKGLVGAYNSTIK	12

<u>ATPG_DROME</u>	<u> O01666</u>	(90) EPKKLLIAVTSDRGLCGAVHTGVAR	33
<u>O74754</u>		(93) EGKTLMVACSSDKGLCGGIHSSISR	35
<u>Q9NE84</u>		(66) QAKAIYIPVMTNRGSCGALNSNVK	57
<u>O21267</u>		(66) VNNKIVVPISSDRGLCGGINTNVK	22
<u>Q9G8R3</u>		(62) DLNYLVLSITVDKSCCGPHNGNVLK	100
<u>O50141</u>		(72) KNSVLLIVIAGDRGLAGGFNTNVLK	19
<u>O50158</u>		(76) VKKTGYIVITSDKGLVGGYNISKILK	13
<u>O67829</u>		(75) ERNVDVILVTADRGLAGAFNSNVIR	19
<u>O05432</u>		(73) VKKAGYVLITADRGLAGGYNANLIR	12
<u>Q52412</u>		(70) VKKTGYLVITSDRGLAGAYNSNVLR	9
<u>Q9ZJ02</u>		(77) VKKSAYIVITSDRGLVGGYNATILK	14
<u>Q9Z688</u>		(74) SDKKLYIALTSDSLGLCGGFNGAVVT	50
<u>Q9X1U6</u>		(66) GNRDLIVVITSDMGLCGSFNSEILR	25
<u>Q9RQ80</u>		(73) IKRIGLIIVSSDRGLCGSLNSNLFR	11
<u>Q9RQ77</u>		(73) TKKIGIIVIVISTDRGLCGSLNISLFK	13
<u>Q9RQ74</u>		(73) VKKIGIIISTDRGLCGNLNVTLFK	20
<u>Q9RGY2</u>		(102) IKTGFLVVTDGRGLVGSYNNSVIK	15
<u>Q9RFL4</u>		(73) VKRVGFLVVSTDRLCGGLNINLFK	10
<u>Q9RAU1</u>		(75) VKKTGYLVITSDRGLVGSYNSNILK	11
<u>Q9PR14</u>		(71) KDRTLYITINSTMGLAGSYNNVNK	40
<u>Q9PJ20</u>		(81) IKTVDLIFITADKGLCGGFNIKTLK	21
<u>Q9PE84</u>		(74) VKRIGYIVIVISSDRGLAGGLNNNLFR	10
<u>Q9KNH4</u>		(73) AKRVGYIIISTDRGLCGGLNINLFK	12
<u>Q9K6H4</u>		(73) VKKTGYIVIVITSDRGLAGAYNSNLR	9
<u>Q9K4D4</u>		(74) PSRAAVLLLTSDRGLAGAFNSNSIK	17
<u>Q9JXQ1</u>		(74) IRRVGFILITSDKGLCGGLNANVLK	14
<u>Q9JW71</u>		(74) IRRVGFILITSDKGLCGGLNANVLK	14
<u>Q9HT19</u>		(73) VKRVGYIVVSSDRGLCGGLNINLFK	9
<u>Q9FDR6</u>		(73) GKRAAVLVVTSDRGMAGGYNHNVLK	19
<u>Q9FAA4</u>		(73) GKRAAVLVVTSDRGMAGGYNHNVLK	19
<u>Q9CER9</u>		(75) VKKTGYLVITSDRGLVGGYNILK	10
<u>Q9ERA8</u>		(88) KKKHLIIGVSSDRGLCGAIHSSVAK	14
<u>Q9D9D7</u>		(88) KKKHLIIGVSSDRGLCGAIHSSVAK	14

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Block IPB000131C

ID	ATPase_gamma; BLOCK
AC	IPB000131C; distance from previous block=(13,21)
DE	ATP synthase gamma subunit
BL	GKR; width=11; seqs=82; 99.5%=790; strength=997
<u>ATPG_BACFI</u>	<u> P22482</u> (113) YGIIIMGRIGR 100
<u>ATPG_ECOLI</u>	<u> P00837</u> (118) IGSKGVSFFNS 11
<u>ATPG_MYCGA</u>	<u> P33257</u> (113) VGIKLNNSFLRT 49
<u>ATPG_THIFE</u>	<u> P41169</u> (118) VGNKGLGFLRR 24
<u>ATPG_VIBAL</u>	<u> P12990</u> (118) VGSKATAFFKH 28
<u>ATP3_ARATH</u>	<u> Q96250</u> (147) VGEKAKAIMFR 32
<u>ATP3_IPOBA</u>	<u> P26360</u> (150) LGEKAKAQLVR 20
<u>ATPG_ANASP</u>	<u> P12408</u> (120) VGRKAEQYFRR 18
<u>ATPG_SPIPL</u>	<u> P50006</u> (119) VGRKAIQHFTR 15
<u>ATPG_SYNPI1</u>	<u> Q05384</u> (120) VGRKAAQYFQR 11
<u>ATPG_SYNPI6</u>	<u> P08450</u> (120) VGRKAGQYFQR 19
<u>ATPG_SYNY3</u>	<u> P17253</u> (120) VGSKAKQYFGR 14

<u>ATP1</u>	<u>ARATH</u>	<u>Q01908</u>	(169)	VGKKGNSYFLR	10
<u>ATP2</u>	<u>ARATH</u>	<u>Q01909</u>	(179)	VGKKGNAYFSR	10
<u>ATPG</u>	<u>CHLRE</u>	<u>P12113</u>	(153)	VGRKGAQYFAR	18
<u>ATPG</u>	<u>ODOSI</u>	<u>Q06908</u>	(175)	IGKKGITYFQR	12
<u>ATPG</u>	<u>PEA</u>	<u>P28552</u>	(170)	VGRKGNSYFNR	9
<u>ATPG</u>	<u>PHATR</u>	<u>Q41075</u>	(175)	VGKKGIAYFER	13
<u>ATPG</u>	<u>SPIOL</u>	<u>P05435</u>	(160)	IGKKGNTYFIR	16
<u>ATPG</u>	<u>TOBAC</u>	<u>P29790</u>	(173)	VGKKGNSYFIR	12
<u>ATPG</u>	<u>BACCA</u>	<u>P41010</u>	(119)	IGRVGLSFFRK	11
<u>ATPG</u>	<u>BACP3</u>	<u>P09222</u>	(119)	IGRVGLSFFRK	11
<u>ATPG</u>	<u>BUCAI</u>	<u>P57123</u>	(118)	FGLKSLSVFKL	26
<u>ATPG</u>	<u>BUCAP</u>	<u>Q51873</u>	(118)	FGLKSLSVFKL	26
<u>ATPG</u>	<u>MYCGE</u>	<u>P47640</u>	(108)	LGRKNQSFWNK	34
<u>ATPG</u>	<u>MYCPN</u>	<u>Q50330</u>	(108)	LGRKNQSFWNK	34
<u>ATPG</u>	<u>PROMO</u>	<u>P29710</u>	(116)	IGKKGRDYCKK	15
<u>ATPG</u>	<u>RHOBL</u>	<u>P05436</u>	(119)	VGKKGREQLKR	11
<u>ATPG</u>	<u>RHOCA</u>	<u>P72246</u>	(121)	VGKKGRDALRR	11
<u>ATPG</u>	<u>RHORU</u>	<u>P07227</u>	(121)	IGKKGRDGLKR	21
<u>ATPG</u>	<u>RICPR</u>	<u>O50289</u>	(122)	IGKKGYEALKR	21
<u>ATPG</u>	<u>BOVIN</u>	<u>P05631</u>	(133)	VGDKIRSIHLR	24
<u>ATPG</u>	<u>HUMAN</u>	<u>P36542</u>	(133)	IGDKIRGILYR	18
<u>ATPG</u>	<u>RAT</u>	<u>P35435</u>	(108)	IGEKIKSILYR	16
<u>ATPG</u>	<u>KLULA</u>	<u>P49377</u>	(122)	IGDKVKGQLLR	26
<u>ATPG</u>	<u>YEAST</u>	<u>P38077</u>	(143)	IGDKIKMQLLR	21
<u>ATPG</u>	<u>ACEWO</u>	<u>P50005</u>	(114)	VGSRGRDHFRN	23
<u>ATPG</u>	<u>BACME</u>	<u>P20602</u>	(118)	IGRVGRDFVFK	15
<u>ATPG</u>	<u>BACST</u>	<u>P42007</u>	(119)	IGRVGLSFFRK	11
<u>ATPG</u>	<u>BACSU</u>	<u>P37810</u>	(121)	IGRVGRDFKK	11
<u>ATPG</u>	<u>ENTHR</u>	<u>P43452</u>	(130)	IGGTGADFFKA	17
<u>ATPG</u>	<u>HAEIN</u>	<u>P43716</u>	(118)	IGSKGISFFRS	9
<u>ATPG</u>	<u>HELPY</u>	<u>P56082</u>	(126)	IGKKGNEYFSF	12
<u>ATPG</u>	<u>HELPJ</u>	<u>Q9ZK80</u>	(126)	IGKKGNEYFSF	12
<u>ATPG</u>	<u>MYCLE</u>	<u>P45824</u>	(119)	VGRKALNYYTF	18
<u>ATPG</u>	<u>MYCTU</u>	<u>Q10597</u>	(119)	VGRKAQNYYSF	19
<u>ATPG</u>	<u>PASMU</u>	<u>Q9L6B6</u>	(118)	IGSKSINFFQS	17
<u>ATPG</u>	<u>STRLI</u>	<u>P50007</u>	(116)	VGRRGLAHYNF	21
<u>ATPG</u>	<u>STRMU</u>	<u>P95788</u>	(121)	IGGMGSDFFRA	41
<u>ATPG</u>	<u>DROME</u>	<u>O01666</u>	(132)	VGDKSRAILSR	18
<u>O74754</u>			(137)	LGEKVRTQLLR	29
<u>Q9NE84</u>			(105)	LGKRGIESLSK	32
<u>O21267</u>			(111)	VGIKAKDQLQR	16
<u>Q9G8R3</u>			(107)	IGRKAKFFFKK	21
<u>O50141</u>			(117)	IGKKAVEYFEK	15
<u>O50158</u>			(120)	IGGIGADFFKA	24
<u>O67829</u>			(120)	VGRKGFQYFTK	20
<u>Q05432</u>			(115)	VGRKGRDFR	8
<u>Q52412</u>			(115)	IGRVGLSFFRK	11
<u>Q9ZJ02</u>			(122)	IGSVGADFFRA	13
<u>Q9Z688</u>			(116)	VGQKGISYFKR	15
<u>Q9X1U6</u>			(107)	VGLKAINHFKD	30
<u>Q9RQ80</u>			(118)	FGLKSLPVFKL	38
<u>Q9RQ77</u>			(118)	LGSKGVSYFKS	12
<u>Q9RQ74</u>			(118)	LGLKGLSFFKS	13
<u>Q9RGY2</u>			(147)	VGSVGAQFFKK	12
<u>Q9RFL4</u>			(118)	IGSKGVSFFDS	19
<u>Q9RAU1</u>			(120)	LGGTGADFFKA	19
<u>Q9PR14</u>			(110)	IGKKGHDFMRL	30
<u>Q9PJ20</u>			(126)	IGKTGIEYFNF	16

<u>Q9PE84</u>	(119)	IGQKASVFFRR	31
<u>Q9KNH4</u>	(118)	IGSKATAFFNN	21
<u>Q9K6H4</u>	(118)	IGRTGRDLLLKK	27
<u>Q9K4D4</u>	(119)	VGRRGLAHYNF	21
<u>Q9JXQ1</u>	(119)	FGSKGLMACQS	29
<u>Q9JW71</u>	(119)	LGSKGLMACQS	25
<u>Q9HT19</u>	(118)	IGSKGASFFRS	9
<u>Q9FDR6</u>	(118)	TGKKGVDYYKF	25
<u>Q9FAA4</u>	(118)	TGKKGVDYYKF	25
<u>Q9CER9</u>	(120)	LGGTGADFFKA	19
<u>Q9ERA8</u>	(133)	VGEKIKGILYR	18
<u>Q9D9D7</u>	(133)	VGEKIKGILYR	18

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Block IPB000131D

ID	ATPase_gamma; BLOCK
AC	IPB000131D; distance from previous block=(33,72)
DE	ATP synthase gamma subunit
BL	DFP; width=26; seqs=82; 99.5%=1450; strength=1161
ATPG <u>BACFI</u> P22482	(166) DELYVWYNHFVSPITQDVTEMKLLL 40
ATPG <u>ECOLI</u> P00837	(166) DKLYIVSNKFINTMSQVPTISQLLPL 13
ATPG <u>MYCGA</u> P33257	(196) DTLDLINDKFPKNISFEPGVDVIIIPA 100
ATPG <u>MYCGE</u> P47640	(158) DRICMVYTKFKNSLIQQSQLFQVFVFPF 33
ATPG <u>MYCPN</u> Q50330	(158) DRICIIYTQFKNPLIQQHANSFQVFVFPF 37
ATPG <u>PROMO</u> P29710	(164) DEVYLIYNEFISALSTELIVKKLLPI 32
ATPG <u>RHORU</u> P07227	(171) DVCTLVYNRFQSAISQVVTRQQIIPF 27
ATPG <u>RICPR</u> O50289	(170) SNCIIYFNKFKNAMTQIPTKQKILPI 49
ATPG <u>THIFE</u> P41169	(166) DVVYLVSSRFVNTMLQRATVEQLLPV 27
ATPG <u>VIBAL</u> P12990	(166) DRLYVVFNKFVNTMVQQPTIDQLLPL 13
ATPG <u>CHLRE</u> P12113	(201) DKVELVFTKFISLINSNPTIQTLLPM 18
ATPG <u>ANASP</u> P12408	(168) DRIELVYTRFVSLVSSRPVIQTLLPL 13
ATPG <u>SPIPL</u> P50006	(167) DRVELIYTKFVSLISSRPVTQTLPL 13
ATPG <u>SYNP1</u> Q05384	(168) DRVELIYTKFVSLISSKPVVQTLPL 10
ATPG <u>SYNP6</u> P08450	(168) DRVELVYTKFLSLVAVSNPVVQTLPL 16
ATPG <u>SYNY3</u> P17253	(168) DRVELIYTRFVSLISSQPVVQTLFPL 12
ATP1 <u>ARATH</u> Q01908	(217) DKVELLYTKFVSLVKSEPVVIHTLLPL 13
ATP2 <u>ARATH</u> Q01909	(228) DKVELVYTKFVSLVKSDPVIHTLLPL 13
ATPG <u>PEA</u> P28552	(218) DKVELLYTKFVSLVKSNPIIHTLLPL 15
ATPG <u>SPIOL</u> P05435	(208) DKVEMLYTKFVSLVKSDPVIHTLLPL 16
ATPG <u>TOBAC</u> P29790	(221) DKVELLYTKFVSLVKSEPVVIHTLLPL 13
ATPG <u>BACCA</u> P41010	(167) DELYMYYNHVSAIQQEVTERKLLPL 17
ATPG <u>BACP3</u> P09222	(167) DELYMYYNHVSAIQQEVTERKLLPL 17
ATPG <u>BUCAI</u> P57123	(166) DKIFIAYNKFHNMKSQYPTITQLLPF 23
ATPG <u>BUCAP</u> O51873	(166) DRLIFIAYNKFHNLSQLYPKISQLLPL 17
ATPG <u>RHOBL</u> P05436	(169) DVVTIFYNRFQSVISQVPTAQVIPA 24

<u>ATPG RHOM</u>	<u>P72246</u>	(171) DVATIFFSVFQSVISQVPTAKQVIP	49
<u>ATPG ODOSE</u>	<u>Q06908</u>	(222) DAVELLYTKFISLIASSPSARTLIP	18
<u>ATPG PHATR</u>	<u>Q41075</u>	(222) DAVELLYTKFVSLIASSPSIRTLP	21
<u>ATP3 ARATH</u>	<u>Q96250</u>	(194) DALRIVYNKFHSVVAFLPTVSTVLSP	30
<u>ATP3 IPOBA</u>	<u>P26360</u>	(197) DALRIVFNKFQSVVSVFVPTMSTVLSP	25
<u>ATPG BOVIN</u>	<u>P05631</u>	(181) DEGSIIFNRFRSVISYKTEEKPIFSL	22
<u>ATPG HUMAN</u>	<u>P36542</u>	(181) DEGSIIFNKFRSVISYKTEEKPIFSL	22
<u>ATPG RAT</u>	<u>P35435</u>	(156) DEGSIIFNQFKSVISYKTEEKPIFSF	21
<u>ATPG KLULA</u>	<u>P49377</u>	(179) DPISSLSFEPSNKPVFNAAAIEQSPS	78
<u>ATPG YEAST</u>	<u>P38077</u>	(201) DPVSSLSFEPSEKPIFNAKTIEQSPS	90
<u>ATPG ACEWO</u>	<u>P50005</u>	(162) DEVYIAYTKFVSTITQHAQMMKLLPL	17
<u>ATPG BACME</u>	<u>P20602</u>	(166) DELYLYYNHFINTISQEVTEKKLLPL	11
<u>ATPG BACST</u>	<u>P42007</u>	(167) DELYMYYNHYVSAIQQEVTTERKLLPL	17
<u>ATPG BACSU</u>	<u>P37810</u>	(169) DELHLVYNHFVSAITQEVTEKKLLPL	10
<u>ATPG ENTHR</u>	<u>P43452</u>	(178) DELYVCYNHHINSLTSQFRVEKMLPI	20
<u>ATPG HAEIN</u>	<u>P43716</u>	(166) DAVYIAYNKFVNTMSQKPVVQQLVPL	16
<u>ATPG HELPY</u>	<u>P56082</u>	(174) DKVIIIHNGFKNMITQEQIRVKTILPI	23
<u>ATPG HELPJ</u>	<u>Q9ZK80</u>	(174) DKVIIIHNGFKNMITQEQIRVKTILPI	23
<u>ATPG MYCLE</u>	<u>P45824</u>	(173) DELHIVFTEFKSMLSQSTKARRMAPM	23
<u>ATPG MYCTU</u>	<u>Q10597</u>	(180) DELHIVYTEFKSMLSQSAAEHRIAPM	20
<u>ATPG PASMU</u>	<u>Q9L6B6</u>	(166) DVVYLVYNKFINTMSQKPVLEKLIPL	15
<u>ATPG STRLI</u>	<u>P50007</u>	(168) DELHIVYTEFVSMMTQTAVDSRLLPL	18
<u>ATPG STRMU</u>	<u>P95788</u>	(169) DELYVCYSHHINSLTSQVRVEKMLPI	19
<u>ATPG DROME</u>	<u>O01666</u>	(180) TEGKIVYNFKSVVSYQCSTLPIFSG	58
<u>O74754</u>		(185) DRIVLVYNKFASAVSFETVMKNLYTT	69
<u>Q9NE84</u>		(153) DRVHVIFHRCVSAGSQKQCYYNIPSY	91
<u>O21267</u>		(157) DTCYLVYNQFRSVLTQNVIESKIASR	36
<u>Q9G8R3</u>		(153) DRFYIIFNRFYSQFTQKVSYDVCSF	59
<u>O50141</u>		(165) DAVELVYTFVSVMTQEPQHRLILPV	34
<u>O50158</u>		(168) DELYVCYNHHVNSLTSQVRVQQMLPI	16
<u>O67829</u>		(169) DRVYLINNEMVTRASYKPQVRVFLPF	84
<u>O05432</u>		(163) DEVNLINTRFYSPIRQVPMVERLLPI	37
<u>Q52412</u>		(163) DELYMYYNHYVSAIQQEVTTERKLLPL	17
<u>Q9ZJ02</u>		(170) DELYVCYNHHVNSLTSQMRVEQMLPI	24
<u>Q9Z688</u>		(164) GEVHVIYTQFLSTVNQKVEVKKVLPI	35
<u>Q9X1U6</u>		(152) ARVRVIFSRFKNVLIQRPEVHELLPI	35
<u>Q9RQ80</u>		(166) DKIFIAYNEFHNMKSQYPKIIQLLPL	19
<u>Q9RQ77</u>		(166) DKLFLSYNQFKNTLVYIPVIMQLLPL	27
<u>Q9RQ74</u>		(166) DRLFLAYNFKFSTLIQIPSIQLLPL	16
<u>Q9RGY2</u>		(195) DQLYVCYTHVNSLSSAFRVEKMLPI	28
<u>Q9RFL4</u>		(166) DKLYIVSNKFINTMSQVPTISQLLPL	13
<u>Q9RAU1</u>		(168) DELYVCYNHHVNSLVSearmekmlpi	18
<u>Q9PR14</u>		(160) NKICIIYTKFINAITFEVSVIDVLPF	36
<u>Q9PJ20</u>		(174) DEVILVHNGYKNMITQELKINHLPV	41
<u>Q9PE84</u>		(167) DRVYLVYNRFINTMVQKASFQDQLLPL	19
<u>Q9KNH4</u>		(166) DRLYLVFNQFVNTMVQKPKIDQLLPL	14
<u>Q9K6H4</u>		(166) DELYIWYNHFVSPIKQDVTEKKVLPL	18
<u>Q9K4D4</u>		(171) DELHIVYTEFVSMMTQTAVDSRLLPL	18
<u>Q9JXQ1</u>		(167) DRIHLVYSGFVNTMRQEPRMEVLLPI	19
<u>Q9JW71</u>		(167) DRIHLVYSGFVNTMRQEPRMEVLLPI	19
<u>Q9HT19</u>		(166) DRLFVVSNKFVNTMTQKPTVEQLIPL	14
<u>Q9FDR6</u>		(186) DQVHVVYTEFISMLTQNPVVHQLLPV	16
<u>Q9FAA4</u>		(186) DQVHVVYTEFISMLTQNPVVHQLLPV	16
<u>Q9CER9</u>		(168) DELYVCYNHHVNSLVSARMEKMLPI	18
<u>Q9ERA8</u>		(181) DEGSIIFNQFKSVISYKTEEKPIFSL	21
<u>Q9D9D7</u>		(181) DEGSIIFNQFKSVISYKTEEKPIFSL	21
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Block IPB000131E

ID	ATPase_gamma; BLOCK	
AC	IPB000131E; distance from previous block=(13, 74)	
DE	ATP synthase gamma subunit	
BL	NQE; width=53; seqs=82; 99.5%=2428; strength=1518	
ATPG MYCGA P33257	(235) LIESKVCEYASRRNAMDTAAKNADDLYNKYKLLYNQLRQAKITQEINEIVAGA	23
ATPG PROMO P29710	(226) ILENTASEHSARKNAMKNATDNAEDMIKDLTLQYNRERQAAITQEISEIVSGA	15
ATPG RICPR O50289	(233) LLQNIVSEEGARMTAMENATNNANDLISKVLKLNRSRQTIITTELIEIIAGA	31
ATPG THIFE P41169	(233) VIEHLACEQSARMVAMKSASDNAKRMVDDLQLAYNKARQAAITQEIAEISAGA	23
ATPG CHLRE P12113	(301) LQEALASELAARMNAMNNASDNAKEKKGLTVQYNKQRQAKITQELAEIVGGA	15
ATPG ANASP P12408	(259) LQESAASELAARMTAMSNASENAGELIKSLSLSYNKARQAAITQELLEVVGGA	13
ATPG SPIPL P50006	(258) WQESTASELAARMTAMSNA SDN ASDLVKTLTLSYNKARQASITQELLEVVGGA	14
ATPG SYNP1 Q05384	(259) LQEAAS E LAARMTAMNNASDNAQTLIGTLTLSYNKARQAAITQEILEVVAGA	14
ATPG SYNP6 P08450	(259) LQEAAS E LAARMTAMNSASDNA ANALVQLTLVYNKARQAAITQELLEVVGGA	13
ATPG SYNY3 P17253	(259) LQESAASELAARMTAMSNA SDNAGQLIGTLTLSYNKARQAAITQELLEVVGGA	14
ATPG BACCA P41010	(231) LLDAKASEHAARMTAMKNATDNANDVIRTLTLSYNRQAAITQEITEIVAGR	10
ATPG BACFI P22482	(233) LLDAKASEFGARMTAMSAATDNASALIEELTLKFNRQAAITQEITEIVGGA	12
ATPG BACP3 P09222	(230) LLDAKASEHAARMTAMKNATDNANE LIRTLTLSYNRQAAITQEITEIVAGA	8
ATPG BUCAI P57123	(232) ILENIASEHAARMIAMKTATDNGNRIKE LQLVYNKVRQANITQELNEIVSGA	13
ATPG BUCAP O51873	(233) LLENIASEQAARMVAMKTATDNGNRIKE LQLIYNKVRQANITQELTEIVAGA	12
ATPG ECOLI P00837	(232) VVENLASEQAARMVAMKAATDNGGSLIKE LQLVYNKARQASITQELTEIVSGA	12
ATPG VIBAL P12990	(233) VVENLACEQAARMIAMKAATDNATNLIDDLLELVYNKARQAAITQELSEIVGGA	13
ATPG MYCGE P47640	(226) LVETKLCESASRQNAMEATKNAKDLLDKYTLQFNKLQRQNSITEEIIIEVIGGM	27
ATPG MYCPN Q50330	(226) LVETKLCESASRQNAMDAAKNAKDLYEKYSIQFNKLQRQNSITQEIIIEIGGI	26
ATPG RHOBL P05436	(231) LLENAASEQGARMSAMDNATRNAAGDMINKLTIQYNRSRQAAITKELIEIIISGA	10
ATPG RHOCA P72246	(235) LLENNASFNGAQMSAMDNATRNAAGDMIDRLTIEYNRSRQAAITKELIEIIISGA	25
ATPG RHORU P07227	(244) MLESFASEQGARMTAMDNATRNAAGDMIKKLSLTYNRTRQAAITKELIEIIISGA	11
ATP1 ARATH Q01908	(317) LQESLAS E LAARMSAMSSASDNA SDLKKSLSMVNRKQAKITGEILEIVAGA	15
ATP2 ARATH Q01909	(328) LQESLAS E LAARMSNAMSNATDNA VELKKNLTMAYNRARQAKITGEILEIVAGA	15
ATPG PEA P28552	(318) LQESLAS E LAARMSAMSSAFDNASELKTDLTRVYNRATQAKITGEILEIVAGD	37
ATPG SPIOL P05435	(308) LQESLAS E LAARMTAMSNA TDNANE LKKTLSINYNRARQAKITGEILEIVAGA	12
ATPG TOBAC P29790	(321) LQESLAS E LAARMSAMSSATDNATELKKNL SRVYNRQRQAKITGEILEIVAGA	12
ATPG ODOSI Q06908	(314) LQESVASELAARMQSMQSASDNAGDLAKRLSTEYNRQAAVTQEILEIVSGA	23
ATPG PHATR Q41075	(314) LQESVASELAARMQSMQSASDNAGSLAKQLNLEYNRQAAVTQELLEIIISGA	23
ATP3 ARATH Q96250	(266) VLENACSEMGARMSAMDSSRNAGEMLDRLTLTYNRTRQASITTELIEIIISGA	18
ATP3 IPOBA P26360	(269) VLENACSEQGARMSAMDSSRNAGEMLDRLTLTYNRTRQASITTELIEIIISGA	17
ATPG BOVIN P05631	(242) LKESTTSEQSARMTAMDNASKNASEMIDKLT LTFNRTRQAVITKELIEIIISGA	10
ATPG HUMAN P36542	(242) LKESTTSEQSARMTAMDNASKNASEMIDKLT LTFNRTRQAVITKELIEIIISGA	10
ATPG RAT P35435	(217) LKESTTSEQSARMTAMDNASKNASDMIDKLT LTFNRTRQAVITKELIEIIISGA	10
ATPG KLULA P49377	(233) MAEGYAAEV SARRNAMDNASKNAGDMIN SYSIL YNRTRQAVITNELVDIITGA	22
ATPG YEAST P38077	(255) MAQGYAAEISARRNAMDNASKNAGDMIN RY SIL YNRTRQAVITNELVDIITGA	23
ATPG ACEWO P50005	(245) MIESAASEQGARRTAMESATTNANE MIDGLTLQYNRVRQAPITQEISEIVGGA	18
ATPG BACME P20602	(229) LLDGKASEHAARMTAMKSATDNAKDLINNLTL SYN RQAAITQEITEIVGGA	9
ATPG BACST P42007	(231) LLDAKASEHAARMTAMKNATDNANDVIRTLTLSYNRQAAITQEITEIVAGR	10
ATPG BACSU P37810	(234) LLDSKASEHAARMTAMKNATDNA KELIDSLSYNRQAAITQEITEIVGGA	8
ATPG ENTHR P43452	(244) IVDAKTAEHAAGMTAMKTATDNAATI IDDLTVSYNRQGAITQEITEIVAGA	20

ATPG HAEIN	P43716	(234) VVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGA	11
ATPG HELPY	P56082	(245) LIDSLAAEHSARMQAMDTATNNAKDLVKTLTISYNKARQEAITTELVEINAGV	16
ATPG HELPJ	Q9ZK80	(245) LIDSLAAEHSARMQAMDTATNNAKDLVKTLTISYNKARQEAITTELVEINAGV	16
ATPG MYCLE	P45824	(239) MLESAASELASRQRAMKSATDNADDLIKALTLEANRERQAQITQEISEIVGGA	14
ATPG MYCTU	Q10597	(246) LLESAASELASRQRAMKSATDNADDLIKALTLMANRERQAQITQEISEIVGGA	16
ATPG PASMU	Q9L6B6	(234) AVENLASEQAARMVAMKAATDNAGNLINEQLVYNKARQASITNELNEIVAGA	13
ATPG STRLI	P50007	(238) LLQSAASKHAATRRAMKSATDNAGELINTSLRLANAARQAEITQEISEIVGGA	22
ATPG STRMU	P95788	(236) IIDAKTAEHAAAGMTAMQTATDNADKVIEDLTKLYNVRQAAITQEITEIVAGA	17
ATPG DROME	O01666	(241) MKEGACSEQSSRMTAMDKNAGEMIDKLTTFNRTQAVITRELIEIISGA	14
O74754		(245) MAEAHCSEMSSRRNAMENASKSAGDMINKFSIQYNRQRQASITNELIDIVTGA	38
Q9NE84		(228) VCENELSEQAARLVAVEGQLSNISTLQQKTSSLYNKTQSSITSSLIEIISAM	100
O21267		(221) LIENVTSSEQGARMNAMDNAKNAGEMIDKLTLYNKNARQASITSELIEIISCA	18
Q9G8R3		(232) LEENEYSALGARATAMNNATKNVSELIDRLRLSYNKNARQETITNELIEIVSCV	42
O50141		(229) IVDSFASEQAARRTAMESASDNANEMIEKSLLYNKNARQAAITQEITEISSAS	19
O50158		(235) IVDAKTAEHAAAGMTAMQTATDNAKVINDLTIQYNKNARQAAITQEITEIVAGA	11
O67829		(233) MVESNAAEHFARMIAMDNATKNAEDLIRQWTLVFNKNARQEAITTELIDITNAV	41
O05432		(226) LLEAKASEHGARMTAMDNATKNAEAMIDKFTLSFNKNARQAAITNEIVEIVAGA	13
Q52412		(226) LLDAKASEHAARMTAMKNATDNANELIRTLTSYNKNARQAAITQEITEIVAGA	8
Q9ZJ02		(237) IIDAKTAENAAGMTAMQTATDNNAKKVISDLTIQYNKNARQAAITQEITEIVAGA	13
Q9Z688		(226) LLNSKASEQASRMSSMDSATKNANDLDDALNICKYRNRIQSAITQEITEIVGGA	27
Q9X1U6		(213) MFQTKIGEYYARQNAMKNATDNAQEVIRELTLAYNKNARQASITQEITEIVTGA	33
Q9RQ80		(232) ILENIASEHAARMMAMKTATENSTERIKELKLLYNKVRQATITQEELTEIIAGA	19
Q9RQ77		(232) ILENCTCEQASRMISMQATDNSEDLIKLRILYNKNARQDNITQEELTEIIISGA	23
Q9RQ74		(231) SLENYTSEQAARMIAMQATDNNSKDLIRELQIYNNKNARQDNITQEELTEIVSGA	19
Q9RGY2		(264) ILDAKTAEHASSMTAMQSATDNANDLVSNLTTKLNKNARQAAITQEITEIIISGA	23
Q9RFL4		(232) VVENLASEQAARMVAMKAATDNCGGSLIKEQLVYNKNARQASITQEELTEIVSGA	12
Q9RAU1		(234) IVDAKTAEHAAAGMTAMRTATDNASHVINDLTIQYNKNARQASITQEITEIVAGA	14
Q9PR14		(232) LIESKISENASRRNAMDAATKNAKALAENYKLINYNTLRQGKIREITEIVAGS	29
Q9PJ20		(238) LIDSLAAEHSARMQAMDNATNNAKARVKQLNLYNKNARQESITTELIEIISGV	16
Q9PE84		(232) MLENIASEHAARMVAMKAASDNANKLIGTLQLVYNKNARQAAITQEISEIVGGA	11
Q9KNH4		(233) VVENLACEQAARMVAMKAATDNASNLLDDQLVYNKNARQAAITQEELTEIVGGA	10
Q9K6H4		(229) LLDAKASEFAARMTAMSAATDNATNLIDEITLTSYNKNARQAAITQEITEIVGGA	10
Q9K4D4		(241) LLQSAASKHAATRRAMKSATDNAGELINTSLRLANAARQAEITQEISEIVGGA	22
Q9JXQ1		(236) LSDNMASEQAARMVAMKAATDNAGNAIKELRVYNKSRQAAITTELSEIVAGA	14
Q9JW71		(236) LSDNMASEQAARMVAMKAATDNAGNAIKELRVYNKSRQAAITTELSEIVAGA	14
Q9HT19		(231) VVENNACEQAARMIAMKNATDNAGELISDLQLIYNNKNARQAAITQEISEIVGGA	11
Q9FDR6		(263) FLEAAAESASRRNAMKSATDNATELVKDLRSRVANQARQAAITQEITEIVGGA	16
Q9FAA4		(263) FLEAAAESASRRNAMKSATDNATELVKDLRSRVANQARQAAITQEITEIVGGA	16
Q9CER9		(234) IVDAKTAEHAAAGMTAMRTATDNASHVINDLTIQYNKNARQASITQEITEIVAGA	14
Q9ERA8		(242) LKESTTSEQSARMTAMDNAKNASDMIDKLTTFNRTQAVITKELIEIIISGA	10
Q9D9D7		(242) LKESTTSEQSARMTAMDNAKNASDMIDKLTTFNRTQAVITKELIEIIISGA	10

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COBBLER sequence (region containing Blocks only)

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COBBLER sequence:

>IPB000131 ATPG_BACME|P20602 from 1 to 285 with embedded consensus blocks
 masLKEIKRIKSVNTQKITKAMKMVAAAKLRKAEqnaksfvpymekiqevvssvalgsrgashpmltarVKKTLYIV
 ITSDRGLCGGYNSNVIKkvspqaeerhqspdeygviaIGKKGMSYFKRrgipvlleitgladqafadiqgiasqtvqmf

adgtfDEVYIIYNKFVNAISQEPTVKQLLPLtdlqpsgk1vgyefepsqeeilev1lpqyaesliyggLLESKASEHAAR
MTAMENATDNAGDLIKKLTLYNRARQAAITQELIEIVSGAaale

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Identification and characterization of the putative transcription-repair-coupling factor gene (trcL) of *Listeria monocytogenes*.

AUTHOR: Zheng W; Kathariou S

AUTHOR ADDRESS: Univ. Hawaii, Honolulu, HI**USA

JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 97 (0):p362 1997

CONFERENCE/MEETING: 97th General Meeting of the American Society for Microbiology Miami Beach, Florida, USA May 4-8, 1997

ISSN: 1060-2011

RECORD TYPE: Citation

LANGUAGE: English

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Physiology

BIOSYSTEMATIC NAMES: Endospore-forming Gram-Positives--Eubacteria, Bacteria; Enterobacteriaceae--Eubacteria, Bacteria; **Pasteurellaceae** --Eubacteria, Bacteria; Regular Nonsporing Gram-Positive Rods--Eubacteria, Bacteria

ORGANISMS: endospore-forming gram-positive rods and cocci (Endospore-forming Gram-Positives); regular nonsporing gram-positive rods (Regular Nonsporing Gram-Positive Rods); *Bacillus subtilis* (Endospore-forming Gram-Positives); *Escherichia coli* (Enterobacteriaceae); **Haemophilus influenzae** (**Pasteurellaceae**); *Listeria monocytogenes* (Regular Nonsporing Gram-Positive Rods

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms

MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; nucleotide sequence

MISCELLANEOUS TERMS: Meeting Abstract; Meeting Poster; CHARACTERIZATION ; CHEMICAL COORDINATION; COLD STRESS; COLD STRESS RESPONSE GENE; FOOD CONTAMINANT; IDENTIFICATION; IN FRAME DELETION MUTANT; LTRA GENE; LTRB GENE; LTRC GENE; MOLECULAR GENETICS; TRANSCRIPTION-REPAIR- COUPLING FACTOR ; TRANSCRIPTION-REPAIR- COUPLING FACTOR GENE; TRCL GENE; TRCL GENE PRODUCT

CONCEPT CODES:

10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10616 External Effects-Temperature as a Primary Variable-Cold (1971-)
23010 Temperature: Its Measurement, Effects and Regulation-Thermodadaptation
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
00520 General Biology-Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals

BIOSYSTEMATIC CODES:

06702 Enterobacteriaceae (1992-)
06703 **Pasteurellaceae** (1992-)
07810 Endospore-forming Gram-Positives (1992-)
07830 Regular Nonsporing Gram-Positive Rods (1992

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ATP synthase gamma subunit signature

PROSITE cross-reference(s)

PS00153; ATPASE GAMMA

Documentation

ATP synthase (proton-translocating ATPase) (EC 3.6.3.14) [1,2] is a component of the cytoplasmic membrane of eubacteria, the inner membrane of mitochondria, and the thylakoid membrane of chloroplasts. The ATPase complex is composed of an oligomeric transmembrane sector, called CF(0), and a catalytic core, called coupling factor CF(1). The former acts as a proton channel; the latter is composed of five subunits, alpha, beta, gamma, delta and epsilon. Subunit gamma is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex. The best conserved region of the gamma subunit [3] is its C-terminus which seems to be essential for assembly and catalysis. As a signature pattern to detect ATPase gamma subunits, we used a 14 residue conserved segment where the last amino acid is found one to three residues from the C-terminal extremity.

Description of pattern(s) and/or profile(s)

Consensus pattern

[IV]-T-X-E-X(2)-[DE]-X(3)-G-A-X-[SAKRW]

Sequences known to belong to this class detected by the pattern

ALL, except for pea chloroplast gamma and two *Bacillus* species gamma.